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217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2009; month=6; day=12; hr=11; min=5; sec=31; ms=874; ]

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Application No: 10559986 Version No: 2.0

**Input Set:****Output Set:**

**Started:** 2009-06-03 17:31:31.594  
**Finished:** 2009-06-03 17:31:37.075  
**Elapsed:** 0 hr(s) 0 min(s) 5 sec(s) 481 ms  
**Total Warnings:** 41  
**Total Errors:** 0  
**No. of SeqIDs Defined:** 95  
**Actual SeqID Count:** 95

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
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W 213	Artificial or Unknown found in <213> in SEQ ID (20)
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W 213	Artificial or Unknown found in <213> in SEQ ID (23)
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W 213	Artificial or Unknown found in <213> in SEQ ID (35)
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**Output Set:**

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Error code	Error Description
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W 402	Undefined organism found in <213> in SEQ ID (52)
W 402	Undefined organism found in <213> in SEQ ID (57)
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W 402	Undefined organism found in <213> in SEQ ID (83)
W 402	Undefined organism found in <213> in SEQ ID (87)



# SEQUENCE LISTING

<110> Nestec S.A.; Cornell Research Foundation, Inc.

<120> Modulation Of Coffee Flavour Precursor Levels In Green Coffee Grains

<130> PAT 60100W-1

<140> 10559986

<141> 2006-09-11

<150> EP 03394056.0

<151> 2003-06-20

<160> 95

<170> PatentIn version 3.5

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<211> 1543

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<221> mRNA

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Met Met Met Thr Ser Gly Gly Leu Met Leu Thr Cys Thr Leu Ala Ile

1 5 10 15

acc ctc tta tcc tgc gca ctc atc tct tca acc act ttc caa cat gaa 217

Thr Leu Leu Ser Cys Ala Leu Ile Ser Ser Thr Thr Phe Gln His Glu

20 25 30

att cag tat cga gta caa gac ccg tta atg ata cgc caa gtc acc gac 265

Ile Gln Tyr Arg Val Gln Asp Pro Leu Met Ile Arg Gln Val Thr Asp

35 40 45

aat cac cac cac cgc cac cac cca ggt agg tct tct gca aac cat cgt 313

Asn His His His Arg His His Pro Gly Arg Ser Ser Ala Asn His Arg

50 55 60



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Leu Leu Gly Thr Thr Thr Glu Val His Phe Lys Ser Phe Val Glu Glu	
65 70 75 80	
tac gag aaa act tac tct acg cac gag gag tac gtg cac cgc ctg ggg	409
Tyr Glu Lys Thr Tyr Ser Thr His Glu Glu Tyr Val His Arg Leu Gly	
85 90 95	
att ttc gcc aag aac ctc atc aag gcc gcg gag cac cag gcc atg gac	457
Ile Phe Ala Lys Asn Leu Ile Lys Ala Ala Glu His Gln Ala Met Asp	
100 105 110	
ccc tcc gca atc cac ggc gtc acc cag ttc tct gat ctc acc gag gag	505
Pro Ser Ala Ile His Gly Val Thr Gln Phe Ser Asp Leu Thr Glu Glu	
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Gly Thr Thr Gln Leu Gly Lys Asp Asp Gly Asp Glu Ser Ala Ala Glu	
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Lys Gly Ala Val Thr Glu Val Lys Thr Gln Gly Arg Cys Gly Ser Cys	
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Thr Gly Lys Leu Leu Ser Leu Ser Glu Gln Gln Leu Val Asp Cys Asp	
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His Met Cys Asp Leu Lys Glu Lys Asp Asp Cys Asp Asp Gly Cys Ser	
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gga ggg cta atg aca act gct ttc aac tac ttg ata gag gca gga ggt	889
Gly Gly Leu Met Thr Thr Ala Phe Asn Tyr Leu Ile Glu Ala Gly Gly	
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aaa ttc aat cct gag aaa gtt gcg gtg aaa gtg cgg aat ttc gca aaa	985
Lys Phe Asn Pro Glu Lys Val Ala Val Lys Val Arg Asn Phe Ala Lys	
275 280 285	
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Ile Pro Glu Asp Glu Ser Gln Ile Ala Ala Asn Val Val His Asn Gly	
290 295 300	
ccg ctt gct att gga ttg aat gcg gta ttc atg caa act tac atc ggg	1081
Pro Leu Ala Ile Gly Leu Asn Ala Val Phe Met Gln Thr Tyr Ile Gly	
305 310 315 320	
ggg gtg tca tgt cct ctt att tgt gac aaa aag agg atc aac cat ggt	1129
Gly Val Ser Cys Pro Leu Ile Cys Asp Lys Lys Arg Ile Asn His Gly	
325 330 335	
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Val Leu Leu Val Gly Tyr Gly Ser Arg Gly Phe Ser Ile Leu Arg Leu	
340 345 350	
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Gly Tyr Lys Pro Tyr Trp Ile Ile Lys Asn Ser Trp Gly Lys Arg Trp	
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Gly Glu His Gly Cys Tyr Arg Leu Cys Arg Gly His Asn Met Cys Gly	
370 375 380	
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Ile Gln Tyr Arg Val Gln Asp Pro Leu Met Ile Arg Gln Val Thr Asp
35 40 45

Asn His His His Arg His His Pro Gly Arg Ser Ser Ala Asn His Arg
50 55 60



Leu Leu Gly Thr Thr Thr Glu Val His Phe Lys Ser Phe Val Glu Glu  
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Tyr Glu Lys Thr Tyr Ser Thr His Glu Glu Tyr Val His Arg Leu Gly  
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Ile Phe Ala Lys Asn Leu Ile Lys Ala Ala Glu His Gln Ala Met Asp  
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Pro Ser Ala Ile His Gly Val Thr Gln Phe Ser Asp Leu Thr Glu Glu  
115 120 125

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Val Met Met Asp Val Ser Asp Leu Pro Glu Ser Phe Asp Trp Arg Glu  
165 170 175

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Trp Ala Phe Ser Thr Thr Gly Ala Ile Glu Gly Ala Asn Phe Ile Ala  
195 200 205

Thr Gly Lys Leu Leu Ser Leu Ser Glu Gln Gln Leu Val Asp Cys Asp  
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His Met Cys Asp Leu Lys Glu Lys Asp Asp Cys Asp Asp Gly Cys Ser  
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Gly Gly Leu Met Thr Thr Ala Phe Asn Tyr Leu Ile Glu Ala Gly Gly  
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Ile Glu Glu Glu Val Thr Tyr Pro Tyr Thr Gly Lys Arg Gly Glu Cys  
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Lys Phe Asn Pro Glu Lys Val Ala Val Lys Val Arg Asn Phe Ala Lys  
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Pro Leu Ala Ile Gly Leu Asn Ala Val Phe Met Gln Thr Tyr Ile Gly  
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Gly Val Ser Cys Pro Leu Ile Cys Asp Lys Lys Arg Ile Asn His Gly  
325 330 335

Val Leu Leu Val Gly Tyr Gly Ser Arg Gly Phe Ser Ile Leu Arg Leu  
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Gly Tyr Lys Pro Tyr Trp Ile Ile Lys Asn Ser Trp Gly Lys Arg Trp  
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Met Ala Lys Pro Ser Ser Ser Leu Leu Thr Leu  
1 5 10

cct tcc ttt ctt ctg atc ttt ttc att ctt gca cta ttt tcc acc acc 159  
Pro Ser Phe Leu Leu Ile Phe Phe Ile Leu Ala Leu Phe Ser Thr Thr  
15 20 25

ctc caa gtt aat gcc ttg gga agg aaa gtg gga gca agg gag aag att 207  
Leu Gln Val Asn Ala Leu Gly Arg Lys Val Gly Ala Arg Glu Lys Ile  
30 35 40



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Glu Asp Val Lys Ser Asn Lys Glu Val Gln Glu Leu Gly Glu Tyr Cys	
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gtt tct gag tac aac aag agt ttg cgg aag aag aac aac gaa agt ggt	303
Val Ser Glu Tyr Asn Lys Ser Leu Arg Lys Lys Asn Asn Glu Ser Gly	
60 65 70 75	
gct cct ata atc ttc aca tct gtg gtg gag gct gag aag cag gtg gtt	351
Ala Pro Ile Ile Phe Thr Ser Val Val Glu Ala Glu Lys Gln Val Val	
80 85 90	
gct ggg atc aaa tat tat ctc aag att aag gcc acc act tct tct ggg	399
Ala Gly Ile Lys Tyr Tyr Leu Lys Ile Lys Ala Thr Thr Ser Ser Gly	
95 100 105	
gtt ccc aag gtt tac gat gcc att gtg gtg gtt cgg cct tgg gtt cat	447
Val Pro Lys Val Tyr Asp Ala Ile Val Val Val Arg Pro Trp Val His	
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act aag cca agg cag ttg ctc aac ttc tcc cct tcc cct gcc act aaa	495
Thr Lys Pro Arg Gln Leu Leu Asn Phe Ser Pro Ser Pro Ala Thr Lys	
125 130 135	
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attattagta cctttcagtg caaattctct ttgctgttaa gtgttcgggtt tttttttttt	608
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Leu Gly Arg Lys Val Gly Ala Arg Glu Lys Ile Glu Asp Val Lys Ser	
35 40 45	
Asn Lys Glu Val Gln Glu Leu Gly Glu Tyr Cys Val Ser Glu Tyr Asn	
50 55 60	



Lys Ser Leu Arg Lys Lys Asn Asn Glu Ser Gly Ala Pro Ile Ile Phe  
65 70 75 80

Thr Ser Val Val Glu Ala Glu Lys Gln Val Val Ala Gly Ile Lys Tyr  
85 90 95

Tyr Leu Lys Ile Lys Ala Thr Thr Ser Ser Gly Val Pro Lys Val Tyr  
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Asp Ala Ile Val Val Val Arg Pro Trp Val His Thr Lys Pro Arg Gln  
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Leu Leu Asn Phe Ser Pro Ser Pro Ala Thr Lys  
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aaaaatccat tcttgaatt catthtatcca tatacaccat acttgtgcat gtcctttttg 180  
gttgttttgc ttttgtgata agtaattgtt ggtttattgg tttttcatga tggctccgga 240  
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tggtattttt gatgtagaag gtaacaataa tgttggtttt gaggtggaac ataaatttaa 360  
agggagaagg aatgagaatg gaggaagagg gtctttttga cttcactcaa ggctcatgat 420  
tcccaccgcc atggcaga atg ctt gca gcc ctt gac atg cct ttg ggt ggc 471  
Met Leu Ala Ala Leu Asp Met Pro Leu Gly Gly  
1 5 10  
aat ggt tcc cct aca gat gca gcg ctc tat ttc act aag ctt tcg att 519  
Asn Gly Ser Pro Thr Asp Ala Ala Leu Tyr Phe Thr Lys Leu Ser Ile



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Gly Thr Pro Pro Gln Asp Tyr Tyr Val Gln Val Asp Thr Gly Ser Asp			
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Ile Leu Trp Val Asn Cys Ala Gly Cys Val Arg Cys Pro Lys Lys Ser			
45	50	55	
agt ctt ggt att gac ttg act cta tat gac atg aaa gcc tcc agc acc			663
Ser Leu Gly Ile Asp Leu Thr Leu Tyr Asp Met Lys Ala Ser Ser Thr			
60	65	70	75
ggg aga ctt gtt act tgt gat caa gac ttt tgc ttg tct gca ttc aat			711
Gly Arg Leu Val Thr Cys Asp Gln Asp Phe Cys Leu Ser Ala Phe Asn			
80	85	90	
gcc cca gcc tct gat tgc aag gtt ggt aac ccc tgt gca tat tct gtt			759
Ala Pro Ala Ser Asp Cys Lys Val Gly Asn Pro Cys Ala Tyr Ser Val			
95	100	105	
act tac gga gac ggg agc tca acc ggc gga tat ttt gtc aga gac tat			807
Thr Tyr Gly Asp Gly Ser Ser Thr Gly Gly Tyr Phe Val Arg Asp Tyr			
110	115	120	
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Ala Lys Leu Asn Gln Leu Thr Gly Asn Leu Gln Thr Ile Pro Met Asn			
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Gly Ser Ile Val Phe Gly Cys Ser Ser Gln Gln Ser Gly Glu Leu Gly			
140	145	150	155
tca tct act gaa gca gtt gat ggc ata att ggt ttt gga caa gca aat			951
Ser Ser Thr Glu Ala Val Asp Gly Ile Ile Gly Phe Gly Gln Ala Asn			
160	165	170	
tca tct att att tca cag ctt gct tca gca gga aag gtt aaa aaa ata			999
Ser Ser Ile Ile Ser Gln Leu Ala Ser Ala Gly Lys Val Lys Lys Ile			
175	180	185	
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Phe Ser His Cys Leu Asp Gly Ile Asn Gly Gly Gly Ile Phe Ala Ile			
190	195		